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SEQUENCE LISTING

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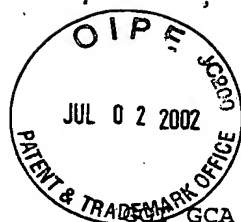
(1) GENERAL INFORMATION:

- (i) APPLICANT: ANDERSON, Darrell R.
HANNA, Nabil
BRAMS, Peter
- (ii) TITLE OF INVENTION: IDENTIFICATION OF UNIQUE BINDING
INTERACTIONS BETWEEN CERTAIN ANTIBODIES AND THE HUMAN B7.1
AND B7.2 CO-STIMULATORY ANTIGENS
- (iii) NUMBER OF SEQUENCES: 6
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
 - (B) STREET: P.O. Box 1404
 - (C) CITY: Alexandria
 - (D) STATE: Virginia
 - (E) COUNTRY: United States
 - (F) ZIP: 22313-1404
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/746,361
 - (B) FILING DATE: 08-NOV-1996
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/487,550
 - (B) FILING DATE: 07-JUN-1995
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Teskin, Robin L.
 - (B) REGISTRATION NUMBER: 35,030
 - (C) REFERENCE/DOCKET NUMBER: 012712-256
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (703) 836-6620
 - (B) TELEFAX: (703) 836-2021

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 705 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..705
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG AGG GTC CCC GCT CAG CTC CTG GGG CTC CTG CTG CTC TGG CTC CCA
Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Trp Leu Pro
1 5 10 15



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HC1

GCA	CGA	TGT	GCC	TAT	GAA	CTG	ACT	CAG	CCA	CCC	TCG	GTG	TCA	GTG	96
Gly	Ala	Arg	Cys	Ala	Tyr	Glu	Leu	Thr	Gln	Pro	Pro	Ser	Val	Ser	Val
			20					25					30		
TCC	CCA	GGA	CAG	ACG	GCC	AGG	ATC	ACC	TGT	GGG	GGA	GAC	AAC	AGT	AGA
Ser	Pro	Gly	Gln	Thr	Ala	Arg	Ile	Thr	Cys	Gly	Gly	Asp	Asn	Ser	Arg
		35					40					45			144
AAT	GAA	TAT	GTC	CAC	TGG	TAC	CAG	CAG	AAG	CCA	GCG	CGG	GCC	CCT	ATA
Asn	Glu	Tyr	Val	His	Trp	Tyr	Gln	Gln	Lys	Pro	Ala	Arg	Ala	Pro	Ile
	50					55					60				192
CTG	GTC	ATC	TAT	GAT	GAT	AGT	GAC	CGG	CCC	TCA	GGG	ATC	CCT	GAG	CGA
Leu	Val	Ile	Tyr	Asp	Asp	Ser	Asp	Arg	Pro	Ser	Gly	Ile	Pro	Glu	Arg
	65				70					75				80	240
TTC	TCT	GGC	TCC	AAA	TCA	GGG	AAC	ACC	GCC	ACC	CTG	ACC	ATC	AAC	GGG
Phe	Ser	Gly	Ser	Lys	Ser	Gly	Asn	Thr	Ala	Thr	Leu	Thr	Ile	Asn	Gly
				85					90					95	288
GTC	GAG	GCC	GGG	GAT	GAG	GCT	GAC	TAT	TAC	TGT	CAG	GTG	TGG	GAC	AGG
Val	Glu	Ala	Gly	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Val	Trp	Asp	Arg
			100					105					110		336
GCT	AGT	GAT	CAT	CCG	GTC	TTC	GGA	GGA	GGG	ACC	CGG	GTG	ACC	GTC	CTA
Ala	Ser	Asp	His	Pro	Val	Phe	Gly	Gly	Gly	Thr	Arg	Val	Thr	Val	Leu
		115					120					125			384
GGT	CAG	CCC	AAG	GCT	GCC	CCC	TCG	GTC	ACT	CTG	TTC	CCG	CCC	TCC	TCT
Gly	Gln	Pro	Lys	Ala	Ala	Pro	Ser	Val	Thr	Leu	Phe	Pro	Pro	Ser	Ser
	130					135					140				432
GAG	GAG	CTT	CAA	GCC	AAC	AAG	GCC	ACA	CTG	GTG	TGT	CTC	ATA	AGT	GAC
Glu	Glu	Leu	Gln	Ala	Asn	Lys	Ala	Thr	Leu	Val	Cys	Leu	Ile	Ser	Asp
	145				150					155					160
TTC	TAC	CCG	GGA	GCC	GTG	ACA	GTG	GCC	TGG	AAG	GCA	GAT	AGC	AGC	CCC
Phe	Tyr	Pro	Gly	Ala	Val	Thr	Val	Ala	Trp	Lys	Ala	Asp	Ser	Ser	Pro
				165					170					175	528
GTC	AAG	GCG	GGA	GTG	GAG	ACC	ACC	ACA	CCC	TCC	AAA	CAA	AGC	AAC	AAC
Val	Lys	Ala	Gly	Val	Glu	Thr	Thr	Thr	Pro	Ser	Lys	Gln	Ser	Asn	Asn
			180					185					190		576
AAG	TAC	GCG	GCC	AGC	AGC	TAC	CTG	AGC	CTG	ACG	CCT	GAG	CAG	TGG	AAG
Lys	Tyr	Ala	Ala	Ser	Ser	Tyr	Leu	Ser	Leu	Thr	Pro	Glu	Gln	Trp	Lys
		195					200					205			624
TCC	CAC	AGA	AGC	TAC	AGC	TGC	CAG	GTC	ACG	CAT	GAA	GGG	AGC	ACC	GTG
Ser	His	Arg	Ser	Tyr	Ser	Cys	Gln	Val	Thr	His	Glu	Gly	Ser	Thr	Val
		210				215					220				672
GAG	AAG	ACA	GTG	GCC	CCT	ACA	GAA	TGT	TCA	TGA					
Glu	Lys	Thr	Val	Ala	Pro	Thr	Glu	Cys	Ser	*					
					225		230			235					705

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATG AAA CAC CTG TGG TTC TTC CTC CTC CTG GTG GCA GCT CCC AGA TGG	48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp	
240 245 250	
GTC CTG TCC GAG GTG AAG CTG CAG CAG TGG GGC GAA GGA CTT CTG CAG	96
Val Leu Ser Glu Val Lys Leu Gln Gln Trp Gly Glu Gly Leu Leu Gln	
255 260 265	
CCT TCG GAG ACC CTG TCC CGC ACC TGC GTT GTC TCT GGT GGC TCC ATC	144
Pro Ser Glu Thr Leu Ser Arg Thr Cys Val Val Ser Gly Gly Ser Ile	
270 275 280	
AGC GGT TAC TAC TAC TGG ACC TGG ATC CGC CAG ACC CCA GGG AGG GGA	192
Ser Gly Tyr Tyr Tyr Trp Thr Trp Ile Arg Gln Thr Pro Gly Arg Gly	
285 290 295	
CTG GAG TGG ATT GGC CAT ATT TAT GGT AAT GGT GCG ACC ACC AAC TAC	240
Leu Glu Trp Ile Gly His Ile Tyr Gly Asn Gly Ala Thr Thr Asn Tyr	
300 305 310 315	
AAT CCC TCC CTC AAG AGT CGA GTC ACC ATT TCA AAA GAC ACG TCC AAG	288
Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Lys Asp Thr Ser Lys	
320 325 330	
AAC CAG TTC TTC CTG AAC TTG AAT TCT GTG ACC GAC GCG GAC ACG GCC	336
Asn Gln Phe Phe Leu Asn Leu Asn Ser Val Thr Asp Ala Asp Thr Ala	
335 340 345	
GTC TAT TAC TGT GCG AGA GGC CCT CGC CCT GAT TGC ACA ACC ATT TGT	384
Val Tyr Tyr Cys Ala Arg Gly Pro Arg Pro Asp Cys Thr Thr Ile Cys	
350 355 360	
TAT GGC GGC TGG GTC GAT GTC TGG GGC CCG GGA GAC CTG GTC ACC GTC	432
Tyr Gly Gly Trp Val Asp Val Trp Gly Pro Gly Asp Leu Val Thr Val	
365 370 375	
TCC TCA GCT AGC ACC AAG GGC CCA TCG GTC TTC CCC CTG GCA CCC TCC	480
Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser	
380 385 390 395	
TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG GGC TGC CTG GTC AAG	528
Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys	
400 405 410	
GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA GGC GCC CTG	576
Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu	
415 420 425	
ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA CTC	624
Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu	
430 435 440	
TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC	672
Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr	
445 450 455	
CAG ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG	720
Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val	
460 465 470 475	

GAC Asp	AAG Lys	AAA Lys	GCA Ala	GAG Glu	CCC Pro	AAA Lys	TCT Ser	TGT Cys	GAC Asp	AAA Lys	ACT Thr	CAC His	ACA Thr	TGC Cys	CCA Pro	768
			480					485						490		
CCG Pro	TGC Cys	CCA Pro	GCA Ala	CCT Pro	GAA Glu	CTC Leu	CTG Leu	GGG Gly	GGA Gly	CCG Pro	TCA Ser	GTC Val	TTC Phe	CTC Leu	TTC Phe	816
			495					500					505			
CCC Pro	CCA Pro	AAA Lys	CCC Pro	AAG Lys	GAC Asp	ACC Thr	CTC Leu	ATG Met	ATC Ile	TCC Ser	CGG Arg	ACC Thr	CCT Pro	GAG Glu	GTC Val	864
		510					515					520				
ACA Thr	TGC Cys	GTG Val	GTG Val	GTG Val	GAC Asp	GTG Ser	AGC His	CAC Glu	GAA Asp	GAC Pro	CCT Glu	GTC Val	AAG Lys	TTC Phe		912
	525					530				535						
AAC Asn	TGG Trp	TAC Tyr	GTG Val	GAC Asp	GGC Gly	GTG Val	GAG Glu	GTG Val	CAT His	AAT Asn	GCC Ala	AAG Lys	ACA Thr	AAG Lys	CCG Pro	960
	540				545					550					555	
CGG Arg	GAG Glu	GAG Glu	CAG Gln	TAC Tyr	AAC Asn	AGC Ser	ACG Thr	TAC Tyr	CGT Arg	GTG Val	GTC Val	AGC Ser	GTC Val	CTC Leu	ACC Thr	1008
				560					565					570		
GTC Val	CTG Leu	CAC His	CAG Gln	GAC Asp	TGG Trp	CTG Leu	AAT Asn	GGC Gly	AAG Lys	GAG Glu	TAC Tyr	AAG Lys	TGC Cys	AAG Lys	GTC Val	1056
			575					580					585			
TCC Ser	AAC Asn	AAA Lys	GCC Ala	CTC Leu	CCA Pro	GCC Ala	CCC Pro	ATC Ile	GAG Glu	AAA Lys	ACC Thr	ATC Ile	TCC Ser	AAA Lys	GCC Ala	1104
		590					595					600				
AAA Lys	GGG Gly	CAG Gln	CCC Pro	CGA Arg	GAA Glu	CCA Pro	CAG Gln	GTG Val	TAC Tyr	ACC Thr	CTG Leu	CCC Pro	CCA Pro	TCC Ser	CGG Arg	1152
	605					610					615					
GAT Asp	GAG Glu	CTG Leu	ACC Thr	AAG Lys	AAC Asn	CAG Gln	GTC Val	AGC Ser	CTG Leu	ACC Thr	TGC Cys	CTG Leu	GTC Val	AAA Lys	GGC Gly	1200
	620				625				630						635	
TTC Phe	TAT Tyr	CCC Pro	AGC Ser	GAC Asp	ATC Ile	GCC Ala	GTG Val	GAG Glu	TGG Trp	GAG Glu	AGC Ser	AAT Asn	GGG Gly	CAG Gln	CCG Pro	1248
				640					645					650		
GAG Glu	AAC Asn	AAC Asn	TAC Tyr	AAG Lys	ACC Thr	ACG Thr	CCT Pro	CCC Pro	GTG Val	CTG Leu	GAC Asp	TCC Ser	GAC Asp	GGC Gly	TCC Ser	1296
			655					660					665			
TTC Phe	TTC Phe	CTC Leu	TAC Tyr	AGC Ser	AAG Lys	CTC Leu	ACC Thr	GTG Val	GAC Asp	AAG Lys	AGC Ser	AGG Arg	TGG Trp	CAG Gln	CAG Gln	1344
		670					675					680				
GGG Gly	AAC Asn	GTC Val	TTC Phe	TCA Ser	TGC Cys	TCC Ser	GTG Val	ATG Met	CAT His	GAG Glu	GCT Ala	CTG Leu	CAC His	AAC Asn	CAC His	1392
	685					690					695					
TAC Tyr	ACG Thr	CAG Gln	AAG Lys	AGC Ser	CTC Leu	TCC Ser	CTG Leu	TCT Ser	CCG Pro	GGT Gly	AAA Lys	TGA *				1431
	700				705					710						

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 720 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG AGC CTC CCT GCT CAG CTC CTC GGG CTG CTA TTG CTC TGC GTC CCC	48
Met Ser Leu Pro Ala Gln Leu Leu Gly Leu Leu Leu Cys Val Pro	
480 485 490	
GGG TCC AGT GGG GAA GTT GTG ATG ACT CAG TCT CCA CTG TCC CTT CCC	96
Gly Ser Ser Gly Glu Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro	
495 500 505	
ATC ACA CCT GGA GAG CCG GCC TCC ATC TCC TGT AGG TCT AGT CAA AGC	144
Ile Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser	
510 515 520 525	
CTT AAA CAC AGT AAT GGA GAC ACC TTC CTG AGT TGG TAT CAG CAG AAG	192
Leu Lys His Ser Asn Gly Asp Thr Phe Leu Ser Trp Tyr Gln Gln Lys	
530 535 540	
CCA GGC CAA CCT CCA AGG CTC CTG ATT TAT AAG GTT TCT AAC CGG GAC	240
Pro Gly Gln Pro Pro Arg Leu Leu Ile Tyr Lys Val Ser Asn Arg Asp	
545 550 555	
TCT GGG GTC CCA GAC AGA TTC AGC GGC AGT GGG GCA GGG ACA GAT TTC	288
Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe	
560 565 570	
ACA CTG AAA ATC AGC GCA GTG GAG GCT GAA GAT GTT GGG GTT TAT TTC	336
Thr Leu Lys Ile Ser Ala Val Glu Ala Glu Asp Val Gly Val Tyr Phe	
575 580 585	
TGC GGG CAA GGT ACA AGG ACT CCT CCC ACT TTC GGC GGA GGG ACC AAG	384
Cys Gly Gln Gly Thr Arg Thr Pro Pro Thr Phe Gly Gly Gly Thr Lys	
590 595 600 605	
GTG GAA ATC AAA CGT ACG GTG GCT GCA CCA TCT GTC TTC ATC TTC CCG	432
Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro	
610 615 620	
CCA TCT GAT GAG CAG TTG AAA TCT GGA ACT GCC TCT GTT GTG TGC CTG	480
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu	
625 630 635	
CTG AAT AAC TTC TAT CCC AGA GAG GCC AAA GTA CAG TGG AAG GTG GAT	528
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp	
640 645 650	
AAC GCC CTC CAA TCG GGT AAC TCC CAG GAG AGT GTC ACA GAG CAG GAC	576
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp	
655 660 665	
AGC AAG GAC AGC ACC TAC AGC CTC AGC AGC ACC CTG ACG CTG AGC AAA	624
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys	
670 675 680 685	
GCA GAC TAC GAG AAA CAC AAA GTC TAC GCC TGC GAA GTC ACC CAT CAG	672
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln	
690 695 700	

GGC CTG AGC TCG CCC GTC ACA AAG AGC TTC AAC AGG GGA GAG TGT TGA	720
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys *	
705 710 715	

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATG GGT TGG AGC CTC ATC TTG CTC TTC CTT GTC GCT GTT GCT ACG CGT	48
Met Gly Trp Ser Leu Ile Leu Leu Phe Leu Val Ala Val Ala Thr Arg	
245 250 255	
GTC CAG TGT GAG GTG CAA CTG GTG GAG TCT GGG GGA GGC TTG GTC CAG	96
Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln	
260 265 270	
CCT GGC GGG TCC CTG AGA GTC TCC TGT GCA GTC TCT GGA TTC ACC TTC	144
Pro Gly Gly Ser Leu Arg Val Ser Cys Ala Val Ser Gly Phe Thr Phe	
275 280 285	
AGT GAC CAC TAC ATG TAT TGG TTC CGC CAG GCT CCA GGG AAG GGG CCG	192
Ser Asp His Tyr Met Tyr Trp Phe Arg Gln Ala Pro Gly Lys Gly Pro	
290 295 300	
GAA TGG GTA GGT TTC ATT AGA AAC AAA CCG AAC GGT GGG ACA ACA GAA	240
Glu Trp Val Gly Phe Ile Arg Asn Lys Pro Asn Gly Gly Thr Thr Glu	
305 310 315 320	
TAC GCC GCG TCT GTG AAA GAC AGA TTC ACC ATC TCC AGA GAT GAT TCC	288
Tyr Ala Ala Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser	
325 330 335	
AAA AGC ATC GCC TAT CTG CAA ATG AGC AGC CTG AAA ATC GAG GAC ACG	336
Lys Ser Ile Ala Tyr Leu Gln Met Ser Ser Leu Lys Ile Glu Asp Thr	
340 345 350	
GCC GTC TAT TAC TGT ACT ACA TCC TAC ATT TCA CAT TGT CGG GGT GGT	384
Ala Val Tyr Tyr Cys Thr Thr Ser Tyr Ile Ser His Cys Arg Gly Gly	
355 360 365	
GTC TGC TAT GGA GGT TAC TTC GAA TTC TGG GGC CAG GGC GCC CTG GTC	432
Val Cys Tyr Gly Gly Tyr Phe Glu Phe Trp Gly Gln Gly Ala Leu Val	
370 375 380	
ACC GTC TCC TCA GCT AGC ACC AAG GGC CCA TCG GTC TTC CCC CTG GCA	480
Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala	
385 390 395 400	
CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG GGC TGC CTG	528
Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu	
405 410 415	

GTC	AAG	GAC	TAC	TTC	CCC	GAA	CCG	GTG	ACG	GTG	TCG	TGG	AAC	TCA	GGC	576
Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	
			420					425					430			
GCC	CTG	ACC	AGC	GGC	GTG	CAC	ACC	TTC	CCG	GCT	GTG	CTA	CAG	TCC	TCA	624
Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	
		435					440					445				
GGA	CTC	TAC	TCC	CTC	AGC	AGC	GTG	GTG	ACC	GTG	CCC	TCC	AGC	AGC	TTG	672
Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	
	450					455					460					
GGC	ACC	CAG	ACC	TAC	ATC	TGC	AAC	GTG	AAT	CAC	AAG	CCC	AGC	AAC	ACC	720
Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	
465					470					475					480	
AAG	GTG	GAC	AAG	AAA	GCA	GAG	CCC	AAA	TCT	TGT	GAC	AAA	ACT	CAC	ACA	768
Lys	Val	Asp	Lys	Lys	Ala	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	
				485					490					495		
TGC	CCA	CCG	TGC	CCA	GCA	CCT	GAA	CTC	CTG	GGG	GGA	CCG	TCA	GTC	TTC	816
Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	
			500					505					510			
CTC	TTC	CCC	CCA	AAA	CCC	AAG	GAC	ACC	CTC	ATG	ATC	TCC	CGG	ACC	CCT	864
Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	
		515					520					525				
GAG	GTC	ACA	TGC	GTG	GTG	GTG	GAC	GTG	AGC	CAC	GAA	GAC	CCT	GAG	GTC	912
Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	
	530					535					540					
AAG	TTC	AAC	TGG	TAC	GTG	GAC	GGC	GTG	GAG	GTG	CAT	AAT	GCC	AAG	ACA	960
Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	
545					550					555					560	
AAG	CCG	CGG	GAG	GAG	CAG	TAC	AAC	AGC	ACG	TAC	CGT	GTG	GTC	AGC	GTC	1008
Lys	Pro	Arg	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val		
			565					570					575			
CTC	ACC	GTC	CTG	CAC	CAG	GAC	TGG	CTG	AAT	GGC	AAG	GAG	TAC	AAG	TGC	1056
Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	
			580					585					590			
AAG	GTC	TCC	AAC	AAA	GCC	CTC	CCA	GCC	CCC	ATC	GAG	AAA	ACC	ATC	TCC	1104
Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	
		595					600					605				
AAA	GCC	AAA	GGG	CAG	CCC	CGA	GAA	CCA	CAG	GTG	TAC	ACC	CTG	CCC	CCA	1152
Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	
	610					615					620					
TCC	CGG	GAT	GAG	CTG	ACC	AAG	AAC	CAG	GTC	AGC	CTG	ACC	TGC	CTG	GTC	1200
Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	
625					630					635					640	
AAA	GGC	TTC	TAT	CCC	AGC	GAC	ATC	GCC	GTG	GAG	TGG	GAG	AGC	AAT	GGG	1248
Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	
				645					650					655		
CAG	CCG	GAG	AAC	AAC	TAC	AAG	ACC	ACG	CCT	CCC	GTG	CTG	GAC	TCC	GAC	1296
Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	
			660					665					670			
GGC	TCC	TTC	TTC	CTC	TAC	AGC	AAG	CTC	ACC	GTG	GAC	AAG	AGC	AGG	TGG	1344
Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	
		675					680					685				

CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC	1392
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His	
690 695 700	

AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA TGA	1437
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys *	
705 710 715	

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 711 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
- (A) NAME/KEY: CDS
 - (B) LOCATION: 1..711

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG AGG GTC CCC GCT CAG CTC CTG GGG CTC CTG CTG CTC TGG CTC CCA	48
Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp Leu Pro	
480 485 490 495	
GGT GCA CGA TGT GAG TCT GTC CTG ACA CAG CCG CCC TCA GTG TCT GGG	96
Gly Ala Arg Cys Glu Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly	
500 505 510	
GCC CCA GGG CAG AAG GTC ACC ATC TCG TGC ACT GGG AGC ACC TCC AAC	144
Ala Pro Gly Gln Lys Val Thr Ile Ser Cys Thr Gly Ser Thr Ser Asn	
515 520 525	
ATT GGA GGT TAT GAT CTA CAT TGG TAC CAG CAG CTC CCA GGA ACG GCC	192
Ile Gly Gly Tyr Asp Leu His Trp Tyr Gln Gln Leu Pro Gly Thr Ala	
530 535 540	
CCC AAA CTC CTC ATC TAT GAC ATT AAC AAG CGA CCC TCA GGA ATT TCT	240
Pro Lys Leu Leu Ile Tyr Asp Ile Asn Lys Arg Pro Ser Gly Ile Ser	
545 550 555	
GAC CGA TTC TCT GGC TCC AAG TCT GGT ACC GCG GCC TCC CTG GCC ATC	288
Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ala Ala Ser Leu Ala Ile	
560 565 570 575	
ACT GGG CTC CAG ACT GAG GAT GAG GCT GAT TAT TAC TGC CAG TCC TAT	336
Thr Gly Leu Gln Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr	
580 585 590	
GAC AGC AGC CTG AAT GCT CAG GTA TTC GGA GGA GGG ACC CGG CTG ACC	384
Asp Ser Ser Leu Asn Ala Gln Val Phe Gly Gly Gly Thr Arg Leu Thr	
595 600 605	
GTC CTA GGT CAG CCC AAG GCT GCC CCC TCG GTC ACT CTG TTC CCG CCC	432
Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro	
610 615 620	
TCC TCT GAG GAG CTT CAA GCC AAC AAG GCC ACA CTG GTG TGT CTC ATA	480
Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile	
625 630 635	

AGT GAC TTC TAC CCG GGA GCC GTG ACA GTG GCC TGG AAG GCA GAT AGC	528
Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser	
640 645 650 655	
AGC CCC GTC AAG GCG GGA GTG GAG ACC ACC ACA CCC TCC AAA CAA AGC	576
Ser Pro Val Lys Ala Gly Val Glu Thr Thr Pro Ser Lys Gln Ser	
660 665 670	
AAC AAC AAG TAC GCG GCC AGC AGC TAC CTG AGC CTG ACG CCT GAG CAG	624
Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln	
675 680 685	
TGG AAG TCC CAC AGA AGC TAC AGC TGC CAG GTC ACG CAT GAA GGG AGC	672
Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser	
690 695 700	
ACC GTG GAG AAG ACA GTG GCC CCT ACA GAA TGT TCA TGA	711
Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser *	
705 710 715	

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATG AAA CAC CTG TGG TTC TTC CTC CTC CTG GTG GCA GCT CCC AGA TGG	48
Met Lys His Leu Trp Phe Phe Leu Leu Val Ala Ala Pro Arg Trp	
240 245 250	
GTC CTG TCC CAG GTG CAG CTG CAG GAG TCG GGC CCA GGA CTG GTG AAG	96
Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys	
255 260 265	
CCT TCG GAG ACC CTG TCC CTC ACC TGC GCT GTC TCT GGT GGC TCC ATC	144
Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile	
270 275 280 285	
AGC GGT GGT TAT GGC TGG GGC TGG ATC CGC CAG CCC CCA GGG AAG GGG	192
Ser Gly Gly Tyr Gly Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly	
290 295 300	
CTG GAG TGG ATT GGG AGT TTC TAT AGT AGT AGT GGG AAC ACC TAC TAC	240
Leu Glu Trp Ile Gly Ser Phe Tyr Ser Ser Ser Gly Asn Thr Tyr Tyr	
305 310 315	
AAC CCC TCC CTC AAG AGT CAA GTC ACC ATT TCA ACA GAC ACG TCC AAG	288
Asn Pro Ser Leu Lys Ser Gln Val Thr Ile Ser Thr Asp Thr Ser Lys	
320 325 330	
AAC CAG TTC TCC CTG AAG CTG AAC TCT ATG ACC GCC GCG GAC ACG GCC	336
Asn Gln Phe Ser Leu Lys Leu Asn Ser Met Thr Ala Ala Asp Thr Ala	
335 340 345	

GTG TAT TAC TGT GTG AGA GAT CGT CTT TTT TCA GTT GTT GGA ATG GTT Val Tyr Tyr Cys Val Arg Asp Arg Leu Phe Ser Val Val Gly Met Val 350 355 360 365	384
TAC AAC AAC TGG TTC GAT GTC TGG GGC CCG GGA GTC CTG GTC ACC GTC Tyr Asn Asn Trp Phe Asp Val Trp Gly Pro Gly Val Leu Val Thr Val 370 375 380	432
TCC TCA GCT AGC ACC AAG GGC CCA TCG GTC TTC CCC CTG GCA CCC TCC Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser 385 390 395	480
TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG GGC TGC CTG CTC AAG Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Leu Lys 400 405 410	528
GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA GGC GCC CTG Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu 415 420 425	576
ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA CTC Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu 430 435 440 445	624
TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr 450 455 460	672
CAG ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val 465 470 475	720
GAC AAG AAA GCA GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA Asp Lys Lys Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro 480 485 490	768
CCG TGC CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe 495 500 505	816
CCC CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val 510 515 520 525	864
ACA TGC GTG GTG GTG GAC GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe 530 535 540	912
AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro 545 550 555	960
CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC GTC CTC ACC Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr 560 565 570	1008
GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG GTC Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val 575 580 585	1056
TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala 590 595 600 605	1104
AAA GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg 610 615 620	1152

GAT Asp	GAG Glu	CTG Leu	ACC Thr 625	AAG Lys	AAC Asn	CAG Gln	GTC Val	AGC Ser 630	CTG Leu	ACC Thr	TGC Cys	CTG Leu	GTC Val 635	AAA Lys	GGC Gly	1200
TTC Phe	TAT Tyr	CCC Pro 640	AGC Ser	GAC Asp	ATC Ile	GCC Ala	GTG Val 645	GAG Glu	TGG Trp	GAG Glu	AGC Ser	AAT Asn 650	GGG Gly	CAG Gln	CCG Pro	1248
GAG Glu	AAC Asn 655	AAC Asn	TAC Tyr	AAG Lys	ACC Thr	ACG Thr 660	CCT Pro	CCC Pro	GTG Val	CTG Leu	GAC Asp 665	TCC Ser	GAC Asp	GGC Gly	TCC Ser	1296
TTC Phe 670	TTC Phe	CTC Leu	TAC Tyr	AGC Ser	AAG Lys 675	CTC Leu	ACC Thr	GTG Val	GAC Asp	AAG Lys 680	AGC Ser	AGG Arg	TGG Trp	CAG Gln 685	CAG Gln	1344
GGG Gly	AAC Asn	GTC Val	TTC Phe	TCA Ser 690	TGC Cys	TCC Ser	GTG Val	ATG Met	CAT His 695	GAG Glu	GCT Ala	CTG Leu	CAC His	AAC Asn 700	CAC His	1392
TAC Tyr	ACG Thr	CAG Gln	AAG Lys 705	AGC Ser	CTC Leu	TCC Ser	CTG Leu 710	TCT Ser 710	CCG Pro	GGT Gly	AAA Lys	TGA *				1431